



TRANSLATE of: raji9-1-1a.seq check: 6400 from: 88 to: 2575
generated symbols 1 to: 829.

Raji9-1-1A HBCK C nfirm ed Sequence
SR4364 Garka/Milne
file:[Bertlesj.Garka]Raji9-1-1A.seq

Raji9-1-1a.Pep Length: 825 [REDACTED] 10:07 Type: P Check: 1271

1 MSAPSEEEY ARLVMEAQPE WLRAEVKRLS HELAETTREK IQAAEYGLAV
51 LEEKHQLKLQ FEELEVDEYA IRSEMEQLKE AFGQAHTNHK KVAADGESRE
101 ESLIQESASK EQYYVRKYLE LQTELKQLRN VLTNTQSENE RLASVAQELK
151 EINQNVETQR GRLRDDIKEY KFREARLLQD YSELEENIS LQKQVSVLRQ
201 NQVEFEGLKH EIKRLEETE YLNSQLEDAI RLKEISERQL EEALETLKTE
251 REQKNSLRKE LSHYMSINDS FYTSHLHVSL DGLKFSDDAA EPNNDAAEALV
301 NGFEHGGLAK LPLDNKTSTP KKEGLAPPSP SLVSDLLSEL NISEIQKLKQ
351 QLMQMEREKA GLLATLQDTQ KQLEHTRGSL SEQQEKVTRL TENLSALRRL
401 QASKERQTAL DNEKDRDSHE DGDYYEVDIN GPEILACKYH VAVAEAGELR
451 EQLKALRSTH EAREAQAHEE KGRYEAEGQA LTEKVSLLK ASRQDRELLA
501 RLEKELKKVS DVAGETQGSL SVAQDELVTF SEELANLYHH VCMCNNETPN
551 RVMLDYREG QGGAGRTSPG GRTSPEARGR RSPILLPKGL LAPEAGRADG
601 GTGDSSPSPG SSLPSPLSDP RREPNIYNL IAIIRDQIKH LQAAVDRTE
651 LSRQRIASQE LGPAVDKDKE ALMEEILKLK SLLSTKREI TLRTVLKAN
701 KQTAEVALAN LSKYENKA MYTETMMKLK NELKALKEDA ATFSSLRAMP
751 ATRCDEYITQ LDEMORQLAA AEDEKKTLS LLRMAIQKL ALTQRLELLE
801 LDHEQTRRGR AKAAPKTKPA TPSL*

Raji9-1-1A HBACK Confirmed Sequence
SR4364 Garka/Milne
file:[Bertlesj.Garka]Raji9-1-1A.seq

Raji9-1-1a.Seq Length: 3345 15:04 Type: N Check:
6400 ..

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1  aaaaagcaaa agaattcgcg gccgcGCGGC TGAGGAGGGC CCGCCTGCG
51  AGAGCCTCAG TGGGAGCCGG CTCAGCCCTC GGCCACCATG TCGGCGCCGT
101 CGGAGGAGGA GGAGTACGCG CGGCTGGTGA TGGAGGCGCA GCCGGAGTGG
151 CTGCGCGCCG AGGTGAAGCG GCTGTCCAC GAGCTGGCCG AGACCACGCG
201 TGAGAAGATC CAGGCGGCCG AGTACGGGCT GCGGTGCTC GAGGAGAAGC
251 ACCAGCTCAA GCTGCAGTTC GAGGAGCTCG AGGTGGACTA TGAGGCTATC
301 CGCAGCGAGA TGGAGCAGCT CAAGGAGGCC TTTGGACAAG CACACACAAA
351 CCACAAGAAG GTGGCTGCTG ACGGAGAGAG CCGGGAGGAG AGCCTGATCC
401 AGGAGTCGGC CTCCAAGGAG CAGTACTACG TCGGAAGGT GCTAGAGCTG
451 CAGACGGAGC TGAAGCAGTT GCGCAATGTC CTCACCAACA CGCAGTCGGA
501 GAATGAGCGC CTGGCCTCTG TGGCCAGGA GCTGAAGGAG ATCAACCAGA
551 ATGTGGAGAT CCAGCGTGGC CGCTGCGGG ATGACATCAA GGAGTACAAA
601 TTCCGGGAAG CTCGTCTGCT GCAGGACTAC TCGGAAGTGG AGGAGGAGAA
651 CATCAGCCTG CAGAAGCAAG TGTCTGTGCT CAGACAGAAC CAGGTGGAGT
701 TTGAGGGCCT CAAGCATGAG ATCAAGCGTC TGGAGGAGGA GACCGAGTAC
751 CTCAACAGCC AGCTGGAGGA TGCCATCCGC CTCAAGGAGA TCTCAGAGCG
801 GCAGCTGGAG GAGGCGCTGG AGACCCTGAA GACGGAGCGC GAACAGAAGA
851 ACAGCCTGCG CAAGGAGCTG TCACACTACA TGAGCATCAA TGACTCCTTC
901 TACACCAGCC ACCTGCATGT CTCGCTGGAT GGCTCAAGT TCAGTGACGA
951 TGCTGCCGAG CCCAACAAACG ATGCCGAGGC CCTGGTCAAT GGCTTTGAGC
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1001 ACGGCGGCTT GGCCAAGCTG CCACTGGACA ACAAGACCTC CACGCCCAAG
1051 AAGGAGGGCC TCGACCGCC CTCCTCCAGC CTCGTCTCCG ACCTACTCAG
1101 TGAGCTCAAC ATCTCTGAGA TCCAGAAGCT GAAGCAGCAG CTGATGCAGA
1151 TGGAGCGGGA AAAGGCGGGC CTGCTGGCAA CGCTGCAGGA CACACAGAAG
1201 CAGCTGGAGC ACACGCGGGG CTCCTGTCA GAACAGCAGG AGAAGGTGAC
1251 CCGCTCACA GAGAATCTGA GTGCCCTGCG GCGCTGCAG GCCAGCAAGG
1301 AGCGGCAGAC AGCCCTGGAC AACGAGAAGG ACCGTGACAG CCATGAGGAT
1351 GGGGACTACT ACGAGGTGGA CATCAACGGG CCTGAGATCT TGGCTGCAA
1401 GTACCATGTG GCTGTGGCTG AGGCTGGCGA GCTCCGCGAG CAGCTCAAGG
1451 CACTGCGCAG CAGCACGAG GCTCGTGAGG CCCAGCACGC CGAGGAGAAG
1501 GGCCGCTATG AGGCTGAGGG CCAGGCACTC ACGGAGAAGG TCTCCTGCT
1551 AGAGAAGGCC AGCCGCCAGG ACCGCGAGCT GCTGGCCCCG CTGGAGAAGG
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1751 ACTACTACCG CGAGGGCCAG GGGGGGGCCG GCCGCACCAG TCCGGGGGGC
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1851 GGGGCTGCTG GCTCCTGAGG CGGGCCGAGC AGATGGTGGG ACGGGGGACA
1901 GCAGCCCCCTC GCCTGGCTCC TCACTGCCAT CACCCCTGAG TGACCCACGC
1951 CGGGAGCCCA TGAACATCTA CAACCTGATC GCTATCATCC GTGACCAGAT
2001 CAAGCACCTG CAGGCAGCCG TGGACCGCAC CACGGAGCTG TCACGCCAGC
2051 GCATTGCCTC TCAGGAGCTG GGGCCCGCCG TGGACAAGGA CAAGGAAGCG
2101 CTTATGGAGG AGATCCTCAA GCTGAAGTCG CTGCTCAGCA CCAAGCGGGA

2151 GCAGATCACC ACGCTGCGCA CTGTGCTCAA GGCCAACAAG CAGACGGCCG
2201 AGGTGGCCCT TGCCAACCTG AAGAGCAAGT ATGAGAATGA GAAGGCCATG
2251 GTTACCGAGA CCATGATGAA GCTGCGCAAT GAGCTCAAGG CCCTCAAGGA
2301 GGACGCGACC ACCTTCTCCT CGCTGCGTGC TATGTTTGCC ACCAGGTGTG
2351 ACGAGTACAT TACACAGCTG GATGAGATGC AGCGGCAGCT GCGGCTGCT
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2451 GAAGCTGGCG CTGACCCAGC GGCTGGAGCT GCTCGAGCTG GACCATGAGC
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2551 CCGAGCTGT AGAGTAGCTG CCAGGAGGAC TTGGCCACCC GGCCCTGTCA
2601 CACTGCGACC CCTTCCCCTT CCCTCTCGTG GCCCACAAGG AGGAAGGAAG
2651 GGCAACCTAA AAGCCCACTT AGAACTTTT TGGATATGCC ACTGCAATTG
2701 TTTTCAAAT AGCATTCCCC AGGTTTTTAA TGGGAGGAAA AAAAGCTTAA
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3001 TCCGCCTCAG CTCCCACCGT GTTTGTCTGG TGTCAGCACG AGGCAGAGCT
3051 GTGTGCTCCA TAGCGTGTAG CTTTAGACTC GGAGATGAGT GCTTTGACCC
3101 AGCGAGGAGC TCAGCTAAGT GTATCCACGC TGTGGTTCAG CAGCCTTTAG
3151 ATCATACGGC ATTGTGGTTC ATGTTTGAAA TTACAGATTT TAAATGCCAT
3201 GTTCATTAAG AAATCCAGGG TATTCAGATT CTGGGGTTTT TCATATTGTA
3251 TTATTATTAT TCTTAGGAAT AGTTCAATGT AACAAGAAGA AAACCTGACC

3301 TTGCTCTGG TTAACAAGT AATAgcggcc gcaattcag ctgg